

primer

201				250	
Prom	WVLTAAHCKK	PNLQV....F	LGKHNLRQRE	SSQEQSSVVR	AVIHPDY... SEQ 10 No. 1
Tadgl4	WVVTAAHCKK	PKYTV....R	LGDHSLQNKD	GPEQEIPVVQ	SIPHPCY... SEQ 10 No. 2
Tryl	WVVSAGHCYK	SRIQV....R	LGEHNIEVLE	GNEQFINAAK	IIRHPQY... SEQ 10 No. 3
Scce	WVLTAAHCKM	NEYTV....H	LGSOTLGDRR	A..QRIKASK	SFRHPGY... SEQ 10 No. 4
Heps	WVLTAAHCFP	ERNRVLSRWR	VFAGAVAQAS	PHGLQLGVQA	VVYHGGYLPF SEQ 10 No. 5

	251			300
Prom	...DAASHDQ	DIMLLRLARP	AKLSELIQPL	PLERDCSA.. NTTSCHILGW
Tadgl4	NSSDVEDHNH	DLMLLQLRDQ	ASLGSKVKPI	SLADHCTQ.. PGQNCVSGW
Tryl	...DRKTLNN	DIMLIKLSRR	AVINARVSTI	SLPTAPPA.. TGTKCLISGW
Scce	ST...QTHVN	DLMLVKLNSQ	ARLSSMVKKV	RLPSRCEP.. PGTTCTVSGW
Heps	RDPNSEENSN	DIALVHLSSP	LPLTEYIQPV	CLPAAGQALV DGKICTVTGW

	301			350
Prom	GKTAD..GDF	PDTIQCAYIH	LVSREECEHA	..YPGQITQN MLCAGDEKYG
Tadgl4	.GTVTSPRENF	PDTLNCAEVK	IFPQKKCEDA	..YPGQITDG MVCAGSSK.G
Tryl	GNTASSGADY	PDELQCLDAP	VLSQAKCEAS	..YPGKITSN MFCVGFLEGG
Scce	GTTTSPDVTF	PSDLMCDVK	LISPQDCTKV	..YKDLENS MLCAGIPDSK
Heps	GNTQYYGQQ.	AGVLQEARVP	IISNDVCNGA	DFYGNQIKPK MFCAGYPEGG

	351	
Prom	KDSCQGDSGG	SEQ 10 No. 1
Tadgl4	ADTCQGDSGG	SEQ 10 No. 2
Tryl	KDSCQGDSGG	SEQ 10 No. 3
Scce	KNACNGDSGG	SEQ 10 No. 4
Heps	IDACQGDSGG	SEQ 10 No. 5

primer

Figure 2. Comparison of amino acid sequence of TADG-14 with known serine protease catalytic domains.

Percent Similarity: 77.220 Percent Identity: 72.201

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

T14pro.Jack x Neur.Jack May 8, 1997 09:27 ..

```
Tadg14 1 MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAAL 50
      ||||| | | . | . ||| ||||| . ||| | : | | ||||| |||||
Neurop 1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50

      51 FQGQQLLCGGVLVGGNWWLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
      ||| : . : ||||| ||||| ||||| ||||| ||||| ||||| |||||
      51 FQGERLICGGVLVGGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100

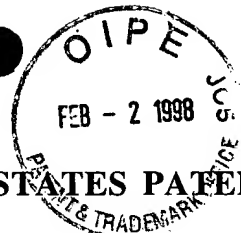
      101 VQSIHPHCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
      ||| ||||| . | . ||| . ||| : ||| . . | . | ||||| : || . | |
      101 AQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQ 150

      151 KCTVSGWGTVTSPRENFPTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
      || : ||||| ||||| . ||||| . ||||| ||||| : | ||| ||||| . : |||||
      151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNK CERAYPGKITEGMVCAG 200

      201 SSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLD 250
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| : : ||||| |||||
      201 SSNGADTCQGDSSGGLVCDGMLQGITSWGS DPCGKPEKPGVYTKICRYTT 250

      251 WIKKIIGSKG 260 SEQ ID No. 7
      ||||| . . :
      251 WIKKTMDNRD 260 SEQ ID No. 10
```

Figure 8. Amino acid homology of TADG-14 with mouse neuropsin.



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: O'Brien, et al.	§	ART UNIT:
	§	1814
FILED: August 21, 1997	§	
	§	EXAMINER:
SERIAL NO.: 08/915,659	§	Jacobson, D.
	§	
FOR: Novel Extracellular Serine	§	
Protease	§	DOCKET: D6020

The Assistant Commissioner of Patents and Trademarks
BOX MISSING PARTS
Washington, DC 20231

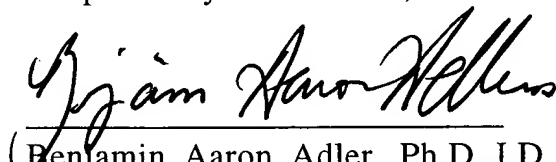
**COMPLIANCE OF REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Dear Sir:

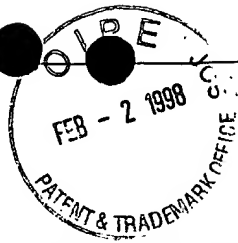
Applicant provides a computer readable form of the Sequence Listing on the enclosed 3.5 inch disk and a paper copy thereof for the above-referenced application. The disk is 1.44 Mb Macintosh-formatted disk. The file is stored as D6020SEQ in text format. I hereby state that the content of the paper copy of the Sequence Listing filed as part of the above-captioned application and the enclosed computer readable copy of the Sequence Listing are the same.

Respectfully submitted,

Date: Jan. 28, 1998


Benjamin Aaron Adler, Ph.D., J.D.
Counsel for Applicant
Registration No. 35,423

McGREGOR & ADLER, P.C.
8011 Candle Lane
Houston, Texas 77071
(713) 777-2321



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: O'Brien et al
- (ii) TITLE OF INVENTION: Novel Extracellular Serine Protease
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
 - (B) STREET: 8011 Candle Lane
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) ZIP: 77071
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 Mb floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh
 - (D) SOFTWARE: Microsoft Word for Macintosh
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/915,659
 - (B) FILING DATE: August 21, 1997
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Benjamin Aaron Adler, Ph.D.
 - (B) REGISTRATION NUMBER: 35,423
 - (C) REFERENCE/DOCKET NUMBER: D6020
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (713) 777-2321

(B) TELEFAX: (713) 777-6908

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1

Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln Val
5 10 15
Phe Leu Glu Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
20 25 30
Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala
35 40 45
Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro
50 55 60
Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp
65 70 75
Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys
80 85 90

Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
 95 100 105
 His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln
 110 115 120
 Ile Thr Gln Asn Met Leu Cys Ala Gln Asp Glu Lys Tyr Gly Lys
 125 130 135
 Asp Ser Cys Gln Gly Asp Ser Gly Gly
 140

(3) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2

Trp Val Val Thr Ala Ala His Cys Lys Lys Pro Lys Tyr Thr Val
 5 10 15
 Arg Leu Gly Asp His Ser Leu Gln Asn Lys Asp Gly Pro Glu Gln
 20 25 30
 Glu Ile Pro Val Val Gln Ser Ile Pro His Pro Cys Tyr Asn Ser
 35 40 45
 Ser Asp Val Glu Asp His Asn His Asp Leu Met Leu Leu Gln Leu
 50 55 60

Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	Val	Lys	Pro	Ile	Ser	Leu
				65					70					75
Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	Asn	Cys	Thr	Val	Ser	Gly
				80					85					90
Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	Asn	Phe	Pro	Asp	Thr	Leu
				95					100					105
Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	Gln	Lys	Lys	Cys	Glu	Asp
				110					115					120
Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	Met	Val	Cys	Ala	Gly	Ser
				125					130					135
Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly		
				140					145					

(4) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 3

Trp	Val	Val	Ser	Ala	Gly	His	Cys	Tyr	Lys	Ser	Arg	Ile	Gln	Val
				5					10					15

Arg Leu Gly Glu His Asn Ile Glu Val Leu Glu Gly Asn Glu Gln
 20 25 30
 Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro Gln Tyr Asp Arg
 35 40 45
 Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys Leu Ser Ser Arg
 50 55 60
 Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu Pro Thr Ala
 65 70 75
 Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp Gly Asn
 80 85 90
 Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys Leu
 95 100 105
 Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
 110 115 120
 Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly
 125 130 135
 Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly
 140 145

(5) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4

Trp Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val
5 10 15
His Leu Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile
20 25 30
Lys Ala Ser Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr
35 40 45
His Val Asn Asp Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg
50 55 60
Leu Ser Ser Met Val Lys Lys Val Arg Leu Pro Ser Arg Cys Glu
65 70 75
Pro Pro Gly Thr Thr Cys Thr Val Ser Gly Trp Gly Thr Thr Thr
80 85 90
Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val
95 100 105
Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Leu
110 115 120
Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Lys
125 130 135
Asn Ala Cys Asn Gly Asp Ser Gly Gly
140

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 5

Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Val
5 10 15
Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Ser
20 25 30
Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gly
35 40 45
Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
50 55 60
Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu
65 70 75
Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val
80 85 90
Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr
95 100 105
Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile
110 115 120
Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln
125 130 135
Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile
140 145 150
Asp Ala Cys Gln Gly Asp Ser Gly Gly
155

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1343 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 6

CTGTAGCAGG CAGAGCTTAC CAAGTCTCTC CGAACTCAAA TGGAAGAAAT ACCTTATGAA 60
TGTAAGAATG TAGGGGGTCA TGGCTTGTA TTTACACAGT GTAAATGAAA CCATCCTAGA 120
GGATTATGAG GAATCCTTTC TATGTGATTT TCAATCATAG CAAGCAAGAA AGGCTCCAGT 180
GTCAAGGTAG TTCAGCTCTT ACAGGATATA AAACAGTCCA TACTTGAGAG AAAAACTTA 240
GATCTGAGTG ATGGAATGTG AAGCAAATCT TTCAAATCA GTAGACATTT CTTGGACATA 300
AAACACAGAT GAGGAAAGGG CTTCAAATTA GAAGTTACGT AATCACCATC AGAAAGTTCA 360
TGTTTGGTAA ATTCTGTTAC TAGAAATGTA GGAAATTCAG GTATAGCTTT GAATCCCAAT 420
TACACATTGG TCAGTGGGAA AACTAAGGGC CTCCAACAGG CAAATTCAGG GAGGATAGGT 480
TTCAGGGAAT GCCCTGGATT CTGGAAGACC TCACCATGGG ACGCCCCCGA CCTCGTGCGG 540
CCAAGACGTG GATGTTCTTG CTCTTGCTGG GGGGAGCCTG GGCAGGACAC TCCAGGGCAC 600
AGGAGGACAA GGTGCTGGGG GGTCATGAGT GCCAACCCCA TTCGCAGCCT TGGCAGGCGG 660
CCTTGTTCCA GGGCCAGCAA CTACTCTGTG GCGGTGTCCT GTAGGTGGC AACTGGGTCC 720
TTACAGCTGC CCACTGTAAA AAACCGAAAT ACACAGTACG CCTGGGAGAC CACAGCCTAC 780
AGAATAAAGA TGGCCAGAG CAAGAAATAC CTGTGGTTCA GTCCATCCCA CACCCTGCT 840
ACAACAGCAG CGATGTGGAG GACCACAACC ATGATCTGAT GCTTCTTCAA CTGCGTGACC 900
AGGCATCCCT GGGGTCCAAA GTGAAGCCCA TCAGCCTGGC AGATCATTGC ACCCAGCCTG 960
GCCAGAAGTG CACCGTCTCA GGCTGGGGCA CTGTCACCAG TCCCCGAGAG AATTTTCCTG 1020
ACACTCTCAA CTGTGCAGAA GTAAAAATCT TTCCCCAGAA GAAGTGTGAG GATGCTTACC 1080
CGGGGCAGAT CACAGATGGC ATGGTCTGTG CAGGCAGCAG CAAAGGGGCT GACACGTGCC 1140
AGGGCGATTG TGGAGGCCCC CTGGTGTGTG ATGGTGCAC TCCAGGGCATC ACATCCTGGG 1200
GCTCAGACCC CTGTGGGAGG TCCGACAAAC CTGGCGTCTA TACCAACATC TGCCGCTACC 1260
TGGACTGGAT CAAGAAGATC ATAGGCAGCA AGGGCTGATT CTAGGATAAG CACTAGATCT 1320
CCCTTAATAA ACTCACGGAA TTC 1343

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 7

Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
5 10 15
Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
20 25 30
Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
35 40 45
Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
50 55 60
Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
65 70 75
Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
80 85 90
Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
95 100 105
His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
110 115 120
Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
125 130 135
Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
 155 160 165
 Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
 170 175 180
 Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
 185 190 195
 Met Val Cys Als Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
 200 205 210
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
 215 220 225
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
 230 235 240
 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
 245 250 255
 Ile Gly Ser Lys Gly
 260

(9) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 8

AGAGGCCACC	ATGGGACGCC	CCCCACCCTG	TGCAATCCAG	CCGTGGATCC	TTCTGCTTCT	60
GTTTCATGGGA	GCGTGGGCAG	GGCTCACCAG	AGCTCAGGGC	TCCAAGATCC	TGGAAGGTCG	120
AGAGTGTATA	CCCCACTCCC	AGCCTTGGCA	GGCAGCCTTG	TTCCAGGGCG	AGAGACTGAT	180
CTGTGGGGGT	GTCCTGGTTG	GAGACAGATG	GGTCCTCACG	GCAGCCCACT	GCAAAAAACA	240
GAAGTACTCC	GTGCGTCTGG	GTGATCATAG	CCTCCAGAGC	AGAGATCAGC	CGGAGCAGGA	300
GATCCAGGTG	GCTCAGTCTA	TCCAGCATCC	TTGCTACAAC	AACAGCAACC	CAGAAGATCA	360
CAGTCACGAT	ATAATGCTCA	TTCGACTGCA	GAAGTCAGCA	AACCTCGGGG	ACAAGGTGAA	420
GCCGGTCCAA	CTGGCCAATC	TGTGTCCCAA	AGTTGGCCAG	AAGTGCATCA	TATCAGGCTG	480
GGGCACTGTC	ACCAGCCCTC	AAGAGAACTT	TCCAAACACC	CTCAACTGTG	CGGAAGTGAA	540
AATCTATTCC	CAGAACAAAGT	GTGAGAGAGC	CTATCCAGGG	AAGATCACCG	AGGTCATGGT	600
CTGTGCTGGC	AGCAGCAATG	GAGCTGACAC	GTGCCAGGGT	GACTCAGGAG	GCCCTCTGGT	660
GTGCGACGGG	ATGCTCCAGG	GCATCACCTC	ATGGGGCTCA	GACCCCTGTG	GGAAACCCGA	720
GAAACCTGGA	GTCTACACCA	AAATCTGCCG	CTACACTACC	TGGATCAAGA	AGACCATGGA	780
CAACAGGGAC	TGATCCTGG					799

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 799 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 9

AGACCTCACC	ATGGGACGCC	CCCACCTCG	TGCGGCCAAG	ACGTGGATGT	TCCTGCTCTT	60
GCTGGGGGGA	GCCTGGGCAG	GACACTCCAG	GGCACAGGAG	GACAAGGTGC	TGGGGGGTCA	120
TGAGTGCCAA	CCCCATTCGC	AGCCTTGGCA	GGCGGCCTTG	TTCCAGGGCC	AGCAACTACT	180
CTGTGGCGGT	GTCCTTGTAG	GTGGCAACTG	GGTCCTTACA	GCTGCCCCACT	GTAAAAAACC	240
GAAATACACA	GTACGCCTGG	GAGACCACAG	CCTACAGAAT	AAAGATGGCC	CAGAGCAAGA	300
AATACCTGTG	GTTTCAGTCCA	TCCACACCC	CTGCTACAAC	AGCAGCGATG	TGGAGGACCA	360
CAACCATGAT	CTGATGCTTC	TTCAACTGCG	TGACCAGGCA	TCCCTGGGGT	CCAAAGTGAA	420

GCCCATCAGC	CTGGCAGATC	ATTGCACCCA	GCCTGGCCAG	AAGTGCACCG	TCTCAGGCTG	480
GGGCACTGTC	ACCAGTCCCC	GAGAGAATTT	TCCTGACACT	CTCAACTGTG	CAGAAGTAAA	540
AATCTTTCCC	CAGAAGAAGT	GTGAGGATGC	TTACCCGGGG	CAGATCACAG	ATGGCATGGT	600
CTGTGCAGGC	AGCAGCAAAG	GGGCTGACAC	GTGCCAGGGC	GATTCTGGAG	GCCCCTGGT	660
GTGTGATGGT	GCACTCCAGG	GCATCACATC	CTGGGGCTCA	GACCCCTGTG	GGAGGTCCGA	720
CAAACCTGGC	GTCTATACCA	ACATCTGCCG	CTACCTGGAC	TGGATCAAGA	AGATCATAGG	780
CAGCAAGGGC	TGATTCTAG					799

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 10

Met	Gly	Arg	Pro	Pro	Pro	Cys	Ala	Ile	Gln	Pro	Trp	Ile	Leu	Leu
				5					10					15
Leu	Leu	Phe	Met	Gly	Ala	Trp	Ala	Gly	Leu	Thr	Arg	Ala	Gln	Gly
				20					25					30
Ser	Lys	Ile	Leu	Glu	Gly	Arg	Glu	Cys	Ile	Pro	His	Ser	Gln	Pro
				35					40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Glu	Arg	Leu	Ile	Cys	Gly	Gly
				50					55					60
Val	Leu	Val	Gly	Asp	Arg	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys Gln Lys Tyr Ser Val Arg Leu Gly Asp His Ser Leu Gln Ser
80 85 90

Arg Asp Gln Pro Glu Gln Glu Ile Gln Val Ala Gln Ser Ile Gln
95 100 105

His Pro Cys Tyr Asn Asn Ser Asn Pro Glu Asp His Ser His Asp
110 115 120

Ile Met Leu Ile Arg Leu Gln Asn Ser Ala Asn Leu Gly Asp Lys
125 130 135

Val Lys Pro Val Gln Leu Ala Asn Leu Cys Pro Lys Val Gly Gln
140 145 150

Lys Cys Ile Ile Ser Gly Trp Gly Thr Val Thr Ser Pro Gln Glu
155 160 165

Asn Phe Pro Asn Thr Leu Asn Cys Ala Glu Val Lys Ile Tyr Ser
170 175 180

Gln Asn Lys Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Glu Gly
185 190 195

Met Val Cys Ala Gly Ser Ser Asn Gly Ala Asp Thr Cys Gln Gly
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Met Leu Gln Gly Ile
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Lys Pro Glu Lys Pro Gly
230 235 240

Val Tyr Thr Lys Ile Cys Arg Tyr Thr Thr Trp Ile Lys Lys Thr
245 250 255

Met asp Asn Arg Asp
260